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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:11:13 ; Search time 45.2571 seconds
(without alignments)
56.115 Million cell updates/sec

Title: US-09-905-691-5

Perfect score: 16

Sequence: 1 CRRARRARRARRAEA 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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- 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	93.8	15	23	Peptide Arg Helix
2	15	93.8	16	23	Peptide Tris-Arg H
3	15	93.8	19	21	Heparin binding pe
4	15	93.8	19	23	Peptide Bis-Arg He
5	9	56.2	19	21	Heparin binding pe
6	9	56.2	92	20	M. tuberculosis an
7	9	56.2	92	20	M. tuberculosis re
8	9	56.2	105	23	M. tuberculosis an
9	9	56.2	160	20	M. tuberculosis an

10	56.2	160	20	AA39043	M. tuberculosis re
11	8	50.0	15	21	Peptide modulating
12	8	50.0	71	22	Protonibacterium
13	8	50.0	262	23	Breast cancer - CA
14	8	50.0	262	23	ABJ10474
15	8	50.0	262	24	Novel human CASB74
16	8	50.0	272	22	Human CASB7439 pro
17	8	50.0	361	23	Protonibacterium
18	8	50.0	361	23	Novel human CASB74
19	7	43.8	617	22	Protonibacterium
20	7	43.8	21	19	Heparin binding pe
21	7	43.8	21	19	Heparin binding pe
22	7	43.8	21	24	H. influenzae Hep
23	7	43.8	47	20	Fragment of human
24	7	43.8	59	22	Protonibacterium
25	7	43.8	107	22	Novel human secret
26	7	43.8	120	22	Human lung tumour
27	7	43.8	120	23	ABU85527
28	7	43.8	120	24	ABU69499
29	7	43.8	120	24	ABU66401
30	7	43.8	121	21	ABU42466
31	7	43.8	124	23	ABG60198
32	7	43.8	161	23	ABP41851
33	7	43.8	162	21	ABG36000
34	7	43.8	202	22	ABG08277
35	7	43.8	205	20	AA41495
36	7	43.8	240	21	AB42380
37	7	43.8	255	22	AAU50234
38	7	43.8	276	22	ABG90891
39	7	43.8	366	24	ABP57738
40	7	43.8	397	24	ABP57732
41	7	43.8	406	22	ABG03776
42	7	43.8	423	22	ABG67125
43	7	43.8	423	22	ABG92579
44	7	43.8	423	24	ABE33211
45	7	43.8	476	24	ABP57745
		669	23	ABB79639	

ALIGNMENTS

RESULT 1

AA39043
ID AAB71432 standard; peptide; 15 AA.

AC AAB71432;

XX 27-NOV-2002 (first entry)

DT Peptide Arg Helix #3 for construction of Tris-Arg helix #3.

DE Sepsis; branched chain peptide; antibacterial; immunosuppressive;
endotoxin; helix peptide.

OS Synthetic.

Key Location/Qualifiers
Modified-site 1

/note= "This residue has a side chain
C(O)-NepsilonH-(CH2)3-Tris-ArgHel#3, where
the Tris-ArgHel#3 is represented in AAB71431"

Modified-site 16
/note= "Acylated residue"

XX EP1232754-A2.

PD 21-AUG-2002.

PF 14-FEB-2002; 2002EP-0251027.

XX M. tuberculosis re

PR 14-FEB-2001; 2001US-268410P.

PA (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.

XX Harris RB, Wolz RL, Wolz G;
PI WPI; 2002-659478/71.
XX Use of cationic helix peptides for treatment of sepsis and for the
PT detection and removal of endotoxins -
PT Disclosure; Fig 2; 18pp; English.
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2,
CC Tetra-Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament
CC for the treatment of sepsis and the detection and removal of endotoxins.
CC The peptides of the invention are used in a method for detecting
CC endotoxin in a sample comprising contacting the sample with a labelled
CC helix peptide and then detecting the presence of any labelled molecule
CC bound to endotoxin. The peptides can also be used in a method for
CC removing endotoxin in a sample which comprises exposing the sample to a
CC helix peptide, bound to a solid support, then collecting the sample. The
CC endotoxin removal may be in vivo, or the peptides may be used to form an
CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
CC removal of endotoxins from plasma fractionation products. They are also
CC used as model frameworks for endotoxin binding from which new analogues
CC may be designed. This sequence represents the peptide Arg Helix #3 which
CC is used in the construction of the branched chain peptide Tris-Arg Helix
CC #3 described in the method of the invention.
XX Sequence 15 AA;
SQ Query Match 93.8%; Score 15; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 RRAAARAARRARAEEA 16
DB 1 RRAAARAARRARAEEA 15
RESULT 2
AAB71430
ID AAB71430 standard; peptide; 16 AA.
XX
AC AAB71430;
XX
DT 27-NOV-2002 (first entry)
XX
DE Peptide Tris-Arg Helix #3 fragment.
XX
KW Sepsis; branched chain peptide; antibacterial; immunosuppressive;
KW endotoxin; helix peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 16
FT /note= "Ala is modified by unidentified R1 group"
XX
PN EP1232754-A2.
XX
PD 21-AUG-2002.
XX
PF 14-FEB-2002; 2002EP-0251027.
XX
PR 14-FEB-2001; 2001US-268410P.
XX
PA (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX
PI Harris RB, Wolz RL, Wolz G;
XX WPI; 2002-659478/71.
XX Use of cationic helix peptides for treatment of sepsis and for the

PT detection and removal of endotoxins -
XX Disclosure; Fig 1B; 18pp; English.
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2,
CC Tetra-Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament
CC for the treatment of sepsis and the detection and removal of endotoxins.
CC The peptides of the invention are used in a method for detecting
CC endotoxin in a sample comprising contacting the sample with a labelled
CC helix peptide and then detecting the presence of any labelled molecule
CC bound to endotoxin. The peptides can also be used in a method for
CC removing endotoxin in a sample which comprises exposing the sample to a
CC helix peptide, bound to a solid support, then collecting the sample. The
CC endotoxin removal may be in vivo, or the peptides may be used to form an
CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
CC removal of endotoxins from plasma fractionation products. They are also
CC used as model frameworks for endotoxin binding from which new analogues
CC may be designed. This sequence represents the peptide Arg Helix #3 which
CC is used in the construction of Tris-Arg Helix #3, a branched chain
CC peptide described in the method of the invention.
XX Sequence 16 AA;
SQ Query Match 93.8%; Score 15; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 RRAAARAARRARAEEA 16
DB 2 RRAAARAARRARAEEA 16
RESULT 3
AAB7840
ID AAB7840 standard; peptide; 19 AA.
XX
AC AAB7840;
XX
DT 01-SEP-2000 (first entry)
XX
DE Heparin binding peptide Bis-Arg helix #2.
XX
KW Heparin binding peptide; antagonist; cardiovascular; coagulant;
KW bleeding wound; vascular anastomoses; leaking prosthetic vascular graft;
KW protamine substitute; treatment.
XX
OS Synthetic.
XX
PN EP999219-A2.
XX
PD 10-MAY-2000.
XX
PF 01-OCT-1999; 99EP-0119514.
XX
PR 06-OCT-1998; 98US-0166930.
XX
PA (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX
PI Harris RB, Sobel M;
XX WPI; 2000-306006/27.
XX
DR New heparin binding molecules, useful for reducing heparin content in a
PT mammal by reducing the anticoagulant effects of heparin -
XX Example 1; Fig 1a; 39pp; English.
XX This invention describes novel heparin binding molecules (I). The
CC molecules (I) are useful as heparin antagonist drugs for cardiovascular
CC application and specifically neutralize heparin's conventional
CC anticoagulant properties. (I) are also useful for counteracting actions
CC of heparin locally e.g. in bleeding wounds, vascular anastomoses or

CC leaking prosthetic vascular grafts. (1) is also useful combined in a
 CC pharmaceutical composition with insulin, as a substitute for protamine
 CC for use in treating diabetics. The heparin binding molecules (1)
 CC specifically neutralize heparin's conventional anticoagulant properties
 CC without causing deleterious hemodynamic side-effects or exacerbation of
 CC the proliferative vascular response to injury. (1) are short-duration,
 CC intravenous drugs to be used in elective or emergency situations which
 CC can safely and specifically neutralize heparin's proliferative response
 CC to injury. This sequence represents a heparin-binding peptide described
 CC in the method of the invention.

XX Sequence 19 AA;
 SQ Query Match 93.8%; Score 15; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRARARARARARAE 16
 Db 5 RRARARARARARAE 19
 |||||

RESULT 4
 AAB71428
 ID AAB71428 standard; peptide; 19 AA.

XX AC AAB71428;
 XX 27-NOV-2002 (first entry)
 XX Peptide Bis-Arg Helix #2 fragment #1.

XX Sepsis; branched chain peptide; antibacterial; immunosuppressive;
 KW endotoxin; helix peptide.
 XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 19 /note= "Ala is modified by unidentified R1 group"
 FT

XX EP1232754-A2.
 XX 21-AUG-2002.
 XX 14-FEB-2002; 2002EP-0251027.
 XX 14-FEB-2001; 2001US-268410P.

XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.

XX Harris RB, Wolz RL, Wolz G;
 XX WPI; 2002-659478/71.

XX Use of cationic helix peptides for treatment of sepsis and for the
 XX detection and removal of endotoxins
 XX Disclosure; Fig 1A; 18pp; English.

XX This invention describes a novel use of antibacterial and
 CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2,
 CC Tetra-Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament
 CC for the treatment of sepsis and the detection and removal of endotoxins.
 CC The peptides of the invention are used in a method for detecting
 CC endotoxin in a sample comprising contacting the sample with a labelled
 CC helix peptide and then detecting the presence of any labelled molecule
 CC bound to endotoxin. The peptides can also be used in a method for
 CC removing endotoxin in a sample which comprises exposing the sample to a
 CC helix peptide, bound to a solid support, then collecting the sample. The
 CC endotoxin removal may be in vivo, or the peptides may be used to form an
 CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
 CC removal of endotoxins from plasma fractionation products. They are also

CC used as model frameworks for endotoxin binding from which new analogues
 CC may be designed. This sequence represents the peptide Arg Helix #2 which
 CC is used in the construction of Bis-Arg Helix #2, a branched chain peptide
 CC described in the method of the invention.

XX Sequence 19 AA;
 SQ Query Match 93.8%; Score 15; DB 23; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRARARARARARAE 16
 Db 5 RRARARARARARAE 19
 |||||

RESULT 5
 AAY87834
 ID AAY87834 standard; peptide; 19 AA.

XX AC AAY87834;
 XX 01-SEP-2000 (first entry)
 XX Heparin binding peptide Arg helix #1.

XX Heparin binding peptide; antagonist; cardiovascular; coagulant;
 KW bleeding wound; vascular anastomoses; leaking prosthetic vascular graft;
 KW protamine substitute; treatment.

XX Synthetic.

XX EP999219-A2.
 XX 10-MAY-2000.

XX 01-OCT-1999; 99EP-0119514.
 XX 06-OCT-1998; 98US-0166930.

XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.

XX Harris RB, Sobel M;
 XX WPI; 2000-306006/27.

XX New heparin binding molecules, useful for reducing heparin content in a
 XX mammal by reducing the anticoagulant effects of heparin.

XX Example 1; Page 7; 39pp; English.

XX This invention describes novel heparin binding molecules (1). The
 CC molecules (1) are useful as heparin antagonist drugs for cardiovascular
 CC application and specifically neutralize heparin's conventional
 CC anticoagulant properties. (1) are also useful for counteracting actions
 CC of heparin locally e.g. in bleeding wounds, vascular anastomoses or
 CC leaking prosthetic vascular grafts. (1) is also useful combined in a
 CC pharmaceutical composition with insulin, as a substitute for protamine
 CC for use in treating diabetics. The heparin binding molecules (1)
 CC specifically neutralize heparin's conventional anticoagulant properties
 CC without causing deleterious hemodynamic side-effects or exacerbation of
 CC the proliferative vascular response to injury. (1) are short-duration,
 CC intravenous drugs to be used in elective or emergency situations which
 CC can safely and specifically neutralize heparin's proliferative response
 CC to injury. This sequence represents a heparin-binding peptide described
 CC in the method of the invention.

XX Sequence 19 AA;
 SQ Query Match 56.2%; Score 9; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AARAAARRA 12
 DE |||||
 DB 4 AARAAARRA 12

RESULT 6
 ID AAY39179 standard; Protein; 92 AA.
 XX
 AC AAY39179;
 DT 05-NOV-1999 (first entry)
 XX
 DE M. tuberculosis antigen 5' MO-4 amino acid sequence.
 XX
 DE Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
 KW immunotherapy; diagnosis; immunisation; vaccine; infection;
 KW immune response; skin test.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9942076-A2.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03268.
 XX
 PR 05-MAY-1998; 98US-0072967.
 PR 18-FEB-1998; 98US-0025157.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
 XX WPI; 1999-527409/44.
 DR N-PSDB; AAZ19371.
 XX
 XX New antigens from Mycobacterium tuberculosis useful in diagnostic
 PT skin tests and protective or therapeutic vaccines or compositions
 XX
 PS Example 5; Page 214; 299pp; English.

CC The present invention describes polypeptides comprising an immunogenic
 CC part of a Mycobacterium tuberculosis antigen (Ag). Also described
 CC are vaccines and fusion protein containing M. tuberculosis Ag's.
 CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and
 CC other polypeptides fragments, can be used in pharmaceutical compositions
 CC or vaccines to generate a protective or therapeutic immune response to
 CC M. tuberculosis and as reagents in skin tests for diagnosis of
 CC tuberculosis. Ag can induce proliferation of, or cytokine secretion
 CC by, T, B or natural killer cells and/or macrophages in
 CC tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to
 CC AAY39225 are used in the exemplification of the present invention.

QY Sequence 92 AA;
 DE
 DE Query Match 56.2%; Score 9; DB 20; Length 92;
 KW Best Local Similarity 100.0%; Pred. No. 0.52;
 KW Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 7 AARAAARRA 15
 DE |||||
 DB 39 AARAAARRA 47

RESULT 7
 ID AAY39036 standard; Protein; 92 AA.
 XX
 AC AAY39036;
 DT 05-NOV-1999 (first entry)
 XX

XX M. tuberculosis recombinant antigen protein MO-4.
 DE
 DE Antigen; diagnosis; detection; infection; antibody; immunisation;
 KW vaccine; immunity.
 KW
 XX Mycobacterium tuberculosis.
 OS
 PN WO9942118-A2.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03265.
 XX
 PR 05-MAY-1998; 98US-0072596.
 PR 18-FEB-1998; 98US-0024753.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
 PI WPI; 1999-527416/44.
 DR
 XX New polypeptide comprising antigenic portions of M. tuberculosis
 PT
 PS Example 5; Page 259; 323pp; English.
 XX
 CC This invention describes novel recombinant antigens and their encoding
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel
 CC polypeptides are useful for detecting M. tuberculosis infection in a
 CC biological sample by detecting antibodies which bind with the
 CC polypeptides, and are useful as vaccines for immunizing against
 CC M. tuberculosis infection. The new detection methods are needed as
 CC current vaccination strategies do not provide 100% immunity.

QY Sequence 92 AA;
 DE
 DE Query Match 56.2%; Score 9; DB 20; Length 92;
 KW Best Local Similarity 100.0%; Pred. No. 0.52;
 KW Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 7 AARAAARRA 15
 DE |||||
 DB 39 AARAAARRA 47

RESULT 8
 ID ABU05688 standard; Protein; 105 AA.
 XX
 AC ABU05688;
 XX
 DT 08-APR-2003 (first entry)
 XX
 DE M. tuberculosis and M. leprae marker protein #339.
 XX
 KW Mycobacterioses; survival; virulence; protective antigen; vaccine;
 KW mycobacterial disease; tuberculosis; leprosy.
 XX
 OS Mycobacterium tuberculosis.
 OS Mycobacterium leprae.
 XX
 PN WO200274903-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-IB01973.
 XX
 PR 22-FEB-2001; 2001US-270123P.
 XX
 XX (INSP) INST PASTEUR.

PN WO200292627-A2.
XX
PD 21-NOV-2002.
XX
PF 07-MAY-2002; 2002WO-EP05011.
XX
PR 16-MAY-2001; 2001GB-0011974.
XX
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX
PI Coche T, Gaulis SRJ, Vinals De Bassols YC;
XX
DR WPI; 2003-120647/11.
DR N-PSDB; AAD51534.
XX
XX
PT Use of a CASB7439 polynucleotide or polypeptide for manufacturing a
PT medicament for immunotherapeutically preventing or treating a patient
PT suffering from or susceptible to preneoplastic lesions of lung cancer
PT and lung cancer
XX
XX Disclosure; Column 74-75; 55pp; English.
XX
XX The invention relates to use of CASB7439 sequences for manufacturing a
CC medicament for immunotherapeutically preventing or treating a patient
CC suffering from or susceptible to preneoplastic lesions of lung cancer,
CC and lung cancer and methods for diagnosing lesions. CASB7439 sequences
CC are useful for manufacturing a medicament for treating preneoplastic
CC lesions of lung cancer and lung cancer, such as SCLC, NSCLC (e.g. large
CC cell (undifferentiated) carcinoma), squamous (epidermoid) carcinoma,
CC carcinoids, adenocarcinoma (including bronchoalveolar), bronchial gland
CC tumours or mesotheliomas. CASB7439 DNA is used in gene therapy. The
CC present sequence is human CASB7439 protein.
XX
SQ Sequence 262 AA;
Query Match 50.0%; Score 8; DB 24; Length 262;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RRAARAAA 9
Db 134 RRAARAAA 141
|||||||
Search completed: August 9, 2003, 16:29:07
Job time : 45.2571 secs